I. Amendments to the Specification

Please amend paragraph [0~~129~~130] as follows: MJB 7/16/09

[0~~129~~130] A majority of the y phage genome (-95%) was sequenced by Genome Therapeutics Corporation (Waltham, Mass.) using a library of 3.0-3.5 kb fragments as templates. This analysis was performed using ABI dye terminator chemistry on automated MegaBace 1000 (Amersham) machines. Base calls and quality scores were determined using the PHRED program (Ewing and Green, 1998 Genome Res. 8:186-194) and reads were assembled by using PHRAP with default program parameters and quality scores. Closure of numerous gaps and determination of the phage termini were accomplished at The Rockefeller University using a primer walking method and purified γDNA as template. At The Rockefeller University samples were thermocycled in an ABI GeneAmp PCR System 9600/9700 and the purified extension products were electrophoresed on an ABI Prism 3700 DNA Analyzer. Sequence data was assembled into a completed contig using the SeqMan program (DNASTAR software package). Putative ORFs were determined by both ORF Finder ~~(www.ncbi/nlm.nih.gov)~~ available through the NCBI and GeneMark approach of gene prediction. ~~(http://opal.biology.gatech.edu/GeneMark/gmhmm2prok.cgi)~~ The BLAST algorithms, available through NCBI, were used for similarity searches of putative ORFs. MJB 7/16/09